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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Oct 01 18:08:24 EDT 2007

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Application No: 10566944 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517
Finished: 2007-09-14 12:26:29.678
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 300	Invalid codon found Ile SEQID (1) POS: 97
E 300	Invalid codon found Glu SEQID (1) POS: 100
E 300	Invalid codon found Asn SEQID (1) POS: 103
E 300	Invalid codon found Tyr SEQID (1) POS: 106
E 300	Invalid codon found Gln SEQID (1) POS: 109
E 300	Invalid codon found Gly SEQID (1) POS: 112
E 300	Invalid codon found Arg SEQID (1) POS: 115
E 300	Invalid codon found Asp SEQID (1) POS: 118
E 300	Invalid codon found Ala SEQID (1) POS: 121
E 300	Invalid codon found Thr SEQID (1) POS: 124
E 300	Invalid codon found Asp SEQID (1) POS: 127
E 300	Invalid codon found Ala SEQID (1) POS: 130
E 300	Invalid codon found Phe SEQID (1) POS: 133
E 300	Invalid codon found Met SEQID (1) POS: 136
E 300	Invalid codon found Val SEQID (1) POS: 139
E 300	Invalid codon found Met SEQID (1) POS: 142
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517
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Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 300	Invalid codon found Leu SEQID (1) POS: 481
E 300	Invalid codon found Val SEQID (1) POS: 484
E 300	Invalid codon found Gly SEQID (1) POS: 487
E 300	Invalid codon found Leu SEQID (1) POS: 490 This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

Input Set:

Output Set :

```
Started: 2007-09-14 12:26:12.517
```

Finished: 2007-09-14 12:26:29.678

Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms

Total Warnings: 108

Total Errors: 281

No. of SeqIDs Defined: 192

Actual SeqID Count: 192

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517
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Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (58)
W 402	Undefined organism found in <213> in SEQ ID (67)
W 402	Undefined organism found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (69)
W 402	Undefined organism found in <213> in SEQ ID (70)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72)
W 402	Undefined organism found in <213> in SEQ ID (73)
W 402	Undefined organism found in <213> in SEQ ID (74)
	This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517
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Total Warnings: 108
Total Errors: 281
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Actual SeqID Count: 192

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (115)
W 213	Artificial or Unknown found in <213> in SEQ ID (116)
W 213	Artificial or Unknown found in <213> in SEQ ID (121)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (121)
W 213	Artificial or Unknown found in <213> in SEQ ID (122)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (122)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (123)
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (124)
W 213	Artificial or Unknown found in <213> in SEQ ID (125)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (126)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (126)
W 213	Artificial or Unknown found in <213> in SEQ ID (127)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (127)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129)

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517
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Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (129)
W 213	Artificial or Unknown found in <213> in SEQ ID (130)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (130)
W 213	Artificial or Unknown found in <213> in SEQ ID (139)
W 213	Artificial or Unknown found in <213> in SEQ ID (140)
W 213	Artificial or Unknown found in <213> in SEQ ID (141)
W 213	Artificial or Unknown found in <213> in SEQ ID (142)
W 213	Artificial or Unknown found in <213> in SEQ ID (143)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (143)
W 213	Artificial or Unknown found in <213> in SEQ ID (144)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (144)
W 213	Artificial or Unknown found in <213> in SEQ ID (145)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (145)
W 213	Artificial or Unknown found in <213> in SEQ ID (146) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (146)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (147)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (148)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (149)

Input Set:

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Started: 2007-09-14 12:26:12.517
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Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (150)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (151)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (152) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Zank, Thorsten
 Bauer, Jorg
 Cirpus, Petra
 Abbadi, Amine
 Heinz, Ernst
 Qiu, Xiao
 Vrinten, Patricia
 Sperling, Petra
 Domergue, Frederic
 Meyer, Astrid
 Kirsch, Jelena

<120> METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN
 TRANSGENIC ORGANISMS

<130> 12810-00193-US

<140> 10566944
 <141> 2007-09-14

<150> DE 103 35 992.3
 <151> 2003-08-01

<150> DE 103 44 557.9
 <151> 2003-09-24

<150> DE 103 47 869.8
 <151> 2003-10-10

<150> DE 103 59 593.7
 <151> 2003-12-18

<150> DE 10 2004 009 457.8
 <151> 2004-02-27

<150> DE 10 2004 012 370.5
 <151> 2004-03-13

<150> DE 10 2004 024 014.0
 <151> 2004-05-14

<160> 192

<170> PatentIn version 3.1

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 <212> DNA
 <213> *Euglena gracilis*

<220>
 <221> CDS
 <222> (1) .. (1266)

<223> delta8-desaturase

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Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr	
1 5 10 15	
tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att	96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile	
20 25 30	
ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg	144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met	
35 40 45	
cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat	192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn	
50 55 60	
ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag	240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu	
65 70 75 80	
gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat	288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp	
85 90 95	
gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt	336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu	
100 105 110	
gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att	384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile	
115 120 125	
ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct	432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser	
130 135 140	
cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac	480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn	
145 150 155 160	
ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca	528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr	
165 170 175	
tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa	576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln	
180 185 190	
ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag	624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu	
195 200 205	

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc	672
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe	
210 215 220	
cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg	720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp	
225 230 235 240	
tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac	768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn	
245 250 255	
caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg	816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu	
260 265 270	
cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc	864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile	
275 280 285	
ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe	
290 295 300	
ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc	960
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile	
305 310 315 320	
ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat	1008
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His	
325 330 335	
gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga	1056
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly	
340 345 350	
ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc	1104
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg	
355 360 365	
cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag	1152
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys	
370 375 380	
cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc	1200
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile	
385 390 395 400	
ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc	1248
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro	
405 410 415	
gcg ggg aag gct cta taa	1266
Ala Gly Lys Ala Leu	

<210> 2

<211> 421

<212> PRT

<213> *Euglena gracilis*

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
 100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
 115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
 130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
 145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
 165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
 180 185 190

Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu	195	200	205
Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe	210	215	220
Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp	225	230	235 240
Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn	245	250	255
Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu	260	265	270
His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile	275	280	285
Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe	290	295	300
Gly	Ile	Ala	Ile	Val	Val	Phe	Met	Asn	His	Tyr	Pro	Leu	Glu	Lys	Ile	305	310	315 320
Gly	Asp	Ser	Val	Trp	Asp	Gly	His	Gly	Phe	Ser	Val	Gly	Gln	Ile	His	325	330	335
Glu	Thr	Met	Asn	Ile	Arg	Arg	Gly	Ile	Ile	Thr	Asp	Trp	Phe	Phe	Gly	340	345	350
Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Trp	Pro	Thr	Leu	Pro	Arg	355	360	365
His	Asn	Leu	Thr	Ala	Val	Ser	Tyr	Gln	Val	Glu	Gln	Leu	Cys	Gln	Lys	370	375	380
His	Asn	Leu	Pro	Tyr	Arg	Asn	Pro	Leu	Pro	His	Glu	Gly	Leu	Val	Ile	385	390	395 400
Leu	Leu	Arg	Tyr	Leu	Ala	Val	Phe	Ala	Arg	Met	Ala	Glu	Lys	Gln	Pro	405	410	415

Ala Gly Lys Ala Leu
420

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<211> 777
<212> DNA
<213> Isochrysis galbana

<220>
<221> CDS
<222> (1)..(777)
<223> delta9-elongase

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Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
130 135 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu

165	170	175	
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg			576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met			
180	185	190	
cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc			624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile			
195	200	205	
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct			672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala			
210	215	220	
ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt			720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe			
225	230	235	240
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag			768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys			
245	250	255	
cag ctc tag			777
Gln Leu			

<210> 4
 <211> 258
 <212> PRT
 <213> Isochrysis galbana

 <400> 4

Met	Ala	Leu	Ala	Asn	Asp	Ala	Gly	Glu	Arg	Ile	Trp	Ala	Ala	Val	Thr
1				5				10						15	

Asp	Pro	Glu	Ile	Leu	Ile	Gly	Thr	Phe	Ser	Tyr	Leu	Leu	Leu	Lys	Pro
		20						25					30		

Leu	Leu	Arg	Asn	Ser	Gly	Leu	Val	Asp	Glu	Lys	Lys	Gly	Ala	Tyr	Arg
	35						40					45			

Thr	Ser	Met	Ile	Trp	Tyr	Asn	Val	Leu	Leu	Ala	Leu	Phe	Ser	Ala	Leu
	50						55				60				

Ser	Phe	Tyr	Val	Thr	Ala	Thr	Ala	Leu	Gly	Trp	Asp	Tyr	Gly	Thr	Gly
65					70					75				80	

Ala	Trp	Leu	Arg	Arg	Gln	Thr	Gly	Asp	Thr	Pro	Gln	Pro	Leu	Phe	Gln
					85				90					95	

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

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Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
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Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
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Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
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Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
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Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
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Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
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gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt      96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
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ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat      144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
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gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt      192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
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ggg ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat      240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
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acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gt

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